REMARKS

Claims 15, 21, 22 and 32-48 are now pending, with claims 15, 21, 22, 32, and 44 being independent.

Claims 1-14, 16-20, and 23-31 have been canceled without prejudice to or disclaimer of the subject matter recited therein.

Claims 32-48 have been added. Support for the sequence identities recited in claims 33, 34, 45 and 46 is found at least in the paragraph at page 6, lines 16-30, of the specification. Support for the use of the term "recombinant" in claims 38, 40, 42, 43 and 48 is found at least in the paragraph at page 10, lines 30-33, of the specification. Support for claims 40-43 are found at least in Examples 5-6, pages 20-23 of the specification. No new matter has been added.

The specification has been amended at two locations to remove reference to the following URL: www.ncbi.nlm.nih.gov/BLAST/.

Claims 15, 21, and 22 have been amended to attend to formal matters, and not for reasons related to patentability. No new matter is believed to be added.

RESPONSE TO RESTRICTION REQUIREMENT

In response to the Restriction Requirement in the Office Action mailed August 9, 2002, Applicants hereby elect, without traverse (claims 1-22, and 28, drawn to nucleic acid sequence encoding the polypeptide of SEQ ID NO:12, the polypeptide, vector, host cell comprising said nucleic acid, transgenic plants and methods of making transgenic plants, classified in Class 800, subclass 295).

Applicants submit that now pending Claims 15, 21, 22 and 32-48 are directed to Group VI.

Please charge any fees or credit any overpayment of fees which are required in connection herewith to Deposit Account No. 04-1928 (E. I. du Pont de Nemours and Company).

In view of the foregoing, allowance of the above-referenced application is respectfully requested.

Respectfully submitted,

J. KENNETH JOUNG
Attorney For Applicants
Registration No. 41,881
Telephone: 302-992-4929
Facsimile: 302-892-1026

Dated: 9 October 2002

VERSION WITH MARKINGS TO SHOW CHANGES MADE

In showing the changes, deleted material is shown within brackets, and inserted material is shown underlined.

IN THE SPECIFICATION:

Paragraph beginning at page 6, line 31, and continuing to page 7, line 15:

A "substantial portion" of an amino acid or nucleotide sequence comprises an amino acid or a nucleotide sequence that is sufficient to afford putative identification of the protein or gene that the amino acid or nucleotide sequence comprises. Amino acid and nucleotide sequences can be evaluated either manually by one skilled in the art, or by using computer-based sequence comparison and identification tools that employ algorithms such as BLAST (Basic Local Alignment Search Tool; Altschul et al. (1993) *J. Mol. Biol. 215*:403-410[; see also www.ncbi.nlm.nih.gov/BLAST/]). In general, a sequence of ten or more contiguous amino acids or thirty or more contiguous nucleotides is necessary in order to putatively identify a polypeptide or nucleic acid sequence as homologous to a known protein or gene. Moreover, with respect to nucleotide sequences, gene-specific oligonucleotide probes comprising 30 or more contiguous nucleotides may be used in sequence-dependent methods of gene identification (e.g., Southern hybridization) and isolation (e.g., *in situ* hybridization of bacterial colonies or bacteriophage plaques). In addition, short oligonucleotides of 12 or more nucleotides may be used as amplification primers in PCR in order to obtain a particular nucleic acid fragment comprising the primers. Accordingly, a "substantial portion" of a nucleotide sequence comprises a nucleotide sequence that will afford specific identification and/or isolation of a nucleic acid fragment comprising the sequence. The instant specification teaches amino acid and nucleotide sequences encoding polypeptides that comprise one or more particular plant proteins. The skilled artisan, having the benefit of the sequences as reported herein, may now use all or a substantial portion of the disclosed sequences for purposes known to those skilled in this art. Accordingly, the instant invention comprises the complete sequences as reported in the accompanying Sequence Listing, as well as substantial portions of those sequences as defined above.

Paragraph at page 17, lines 13-29:

cDNA clones encoding farnesyltransferase subunits were identified by conducting BLAST (Basic Local Alignment Search Tool; Altschul et al. (1993) *J. Mol. Biol. 215*:403-410[; see also www.ncbi.nlm.nih.gov/BLAST/]) searches for similarity

to sequences contained in the BLAST "nr" database (comprising all non-redundant GenBank CDS translations, sequences derived from the 3-dimensional structure Brookhaven Protein Data Bank, the last major release of the SWISS-PROT protein sequence database, EMBL, and DDBJ databases). The cDNA sequences obtained in Example 1 were analyzed for similarity to all publicly available DNA sequences contained in the "nr" database using the BLASTN algorithm provided by the National Center for Biotechnology Information (NCBI). The DNA sequences were translated in all reading frames and compared for similarity to all publicly available protein sequences contained in the "nr" database using the BLASTX algorithm (Gish and States (1993) *Nat. Genet. 3*:266-272) provided by the NCBI. For convenience, the P-value (probability) of observing a match of a cDNA sequence to a sequence contained in the searched databases merely by chance as calculated by BLAST are reported herein as "pLog" values, which represent the negative of the logarithm of the reported P-value. Accordingly, the greater the pLog value, the greater the likelihood that the cDNA sequence and the BLAST "hit" represent homologous proteins.

IN THE CLAIMS:

15. (amended) A method of selecting an isolated polynucleotide that affects the level of expression of a farnesyltransferase polypeptide in a plant cell, the method comprising the steps of:

(a) constructing an isolated polynucleotide comprising a nucleotide sequence of at least [one of] 30 contiguous nucleotides [derived from a nucleotide sequence selected from the group consisting] of SEQ ID NO:11, [1, 3, 5, 7, 9, 11, 13, 15, 17 and the] or a complement of such nucleotide sequence[s], wherein the complement and the nucleotide sequence consist of the same number of nucleotides and are 100% complementary;

(b) introducing the isolated polynucleotide into a plant cell;

(c) measuring the level of farnesyltransferase polypeptide in the plant cell containing the polynucleotide; and

(d) comparing the level of farnesyltransferase polypeptide in the plant cell containing the isolated polynucleotide with the level of farnesyltransferase polypeptide in a plant cell that does not contain the polynucleotide.

21. (amended) A method of obtaining a nucleic acid fragment encoding a substantial portion of a farnesyltransferase gene comprising the steps of:

(a) synthesizing an oligonucleotide primer comprising a nucleotide sequence of at least [one of] 40 contiguous nucleotides [derived from a nucleotide

sequence selected from the group consisting] of SEQ ID NO:11, [1, 3, 5, 7, 9, 11, 13, 15, 17 and the] or a complement of such nucleotide sequence[s], wherein the complement and the nucleotide sequence consist of the same number of nucleotides and are 100% complementary; and

(b) amplifying a nucleic acid sequence using the oligonucleotide primer.

22. (amended) A method of obtaining a nucleic acid fragment encoding all or a substantial portion of the amino acid sequence encoding a farnesyltransferase protein comprising the steps of:

(a) probing a cDNA or genomic library with an isolated polynucleotide comprising a nucleotide sequence of at least [one of] 30 contiguous nucleotides [derived from a nucleotide sequence selected from the group consisting] of SEQ ID NO:11, [1, 3, 5, 7, 9, 11, 13, 15, 17, and the] or a complement of such nucleotide sequence[s], wherein the complement and the nucleotide sequence consist of the same number of nucleotides and are 100% complementary;

(b) identifying a DNA clone that hybridizes with the isolated polynucleotide;

(c) isolating the identified DNA clone; and

(d) optionally sequencing the cDNA or genomic fragment that comprises the isolated DNA clone.